SEQUENCE LISTING

<110> Tamatani, Takuya
Tezuka, Katsunari

<120> CELL SURFACE MOLECULE MEDIATING CELL ADHESION AND SIGNAL TRANSMISSION

<130> 06501-039001

<140> US 09/383,551
<141> 1999-08-26

<150> PCT/JP98/00837
<151> 1998-02-27

<150> JAPAN 09-62290
<151> 1997-02-27

<150> JAPAN 10-62217
<151> 1998-02-26

<160> 26

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 600
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(597)

<400> 1

```
atg aag tca ggc ctc tgg tat ttc ttt ctc ttc tgc ttg cgc att aaa       48
Met Lys Ser Gly Leu Trp Tyr Phe Phe Leu Phe Cys Leu Arg Ile Lys
 1               5                  10                  15

gtt tta aca gga gaa atc aat ggt tct gcc aat tat gag atg ttt ata       96
Val Leu Thr Gly Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile
            20                  25                  30

ttt cac aac gga ggt gta caa att tta tgc aaa tat cct gac att gtc      144
Phe His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val
        35                  40                  45

cag caa ttt aaa atg cag ttg ctg aaa ggg ggg caa ata ctc tgc gat      192
Gln Gln Phe Lys Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp
    50                  55                  60

ctc act aag aca aaa gga agt gga aac aca gtg tcc att aag agt ctg      240
Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu
65                  70                  75                  80
```

```
aaa ttc tgc cat tct cag tta tcc aac aac agt gtc tct ttt ttt cta      288
Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
                 85                  90                  95

tac aac ttg gac cat tct cat gcc aac tat tac ttc tgc aac cta tca      336
Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser
            100                 105                 110

att ttt gat cct cct cct ttt aaa gta act ctt aca gga gga tat ttg      384
Ile Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu
        115                 120                 125

cat att tat gaa tca caa ctt tgt tgc cag ctg aag ttc tgg tta ccc      432
His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro
    130                 135                 140

ata gga tgt gca gcc ttt gtt gta gtc tgc att ttg gga tgc ata ctt      480
Ile Gly Cys Ala Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu
145                 150                 155                 160

att tgt tgg ctt aca aaa aag aag tat tca tcc agt gtg cac gac cct      528
Ile Cys Trp Leu Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro
                165                 170                 175

aac ggt gaa tac atg ttc atg aga gca gtg aac aca gcc aaa aaa tct      576
Asn Gly Glu Tyr Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser
            180                 185                 190

aga ctc aca gat gtg acc cta taa                                     600
Arg Leu Thr Asp Val Thr Leu
        195
```

<210> 2
<211> 199
<212> PRT
<213> Homo sapiens

<400> 2

```
Met Lys Ser Gly Leu Trp Tyr Phe Phe Leu Phe Cys Leu Arg Ile Lys
 1               5                  10                  15
Val Leu Thr Gly Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile
            20                  25                  30
Phe His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val
        35                  40                  45
Gln Gln Phe Lys Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp
    50                  55                  60
Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu
65                  70                  75                  80
Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
                85                  90                  95
Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser
            100                 105                 110
Ile Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu
        115                 120                 125
His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro
    130                 135                 140
```

```
Ile Gly Cys Ala Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu
145                 150                 155                 160
Ile Cys Trp Leu Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro
                165                 170                 175
Asn Gly Glu Tyr Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser
            180                 185                 190
Arg Leu Thr Asp Val Thr Leu
        195
```

<210> 3
<211> 2610
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (26)...(622)

<400> 3

```
ggactgttaa ctgtttctgg caaac atg aag tca ggc ctc tgg tat ttc ttt       52
                            Met Lys Ser Gly Leu Trp Tyr Phe Phe
                             1               5

ctc ttc tgc ttg cgc att aaa gtt tta aca gga gaa atc aat ggt tct      100
Leu Phe Cys Leu Arg Ile Lys Val Leu Thr Gly Glu Ile Asn Gly Ser
 10                  15                  20                  25

gcc aat tat gag atg ttt ata ttt cac aac gga ggt gta caa att tta      148
Ala Asn Tyr Glu Met Phe Ile Phe His Asn Gly Gly Val Gln Ile Leu
                30                  35                  40

tgc aaa tat cct gac att gtc cag caa ttt aaa atg cag ttg ctg aaa      196
Cys Lys Tyr Pro Asp Ile Val Gln Gln Phe Lys Met Gln Leu Leu Lys
            45                  50                  55

ggg ggg caa ata ctc tgc gat ctc act aag aca aaa gga agt gga aac      244
Gly Gly Gln Ile Leu Cys Asp Leu Thr Lys Thr Lys Gly Ser Gly Asn
        60                  65                  70

aca gtg tcc att aag agt ctg aaa ttc tgc cat tct cag tta tcc aac      292
Thr Val Ser Ile Lys Ser Leu Lys Phe Cys His Ser Gln Leu Ser Asn
    75                  80                  85

aac agt gtc tct ttt ttt cta tac aac ttg gac cat tct cat gcc aac      340
Asn Ser Val Ser Phe Phe Leu Tyr Asn Leu Asp His Ser His Ala Asn
 90                  95                  100                 105

tat tac ttc tgc aac cta tca att ttt gat cct cct cct ttt aaa gta      388
Tyr Tyr Phe Cys Asn Leu Ser Ile Phe Asp Pro Pro Pro Phe Lys Val
                110                 115                 120

act ctt aca gga gga tat ttg cat att tat gaa tca caa ctt tgt tgc      436
Thr Leu Thr Gly Gly Tyr Leu His Ile Tyr Glu Ser Gln Leu Cys Cys
            125                 130                 135

cag ctg aag ttc tgg tta ccc ata gga tgt gca gcc ttt gtt gta gtc      484
Gln Leu Lys Phe Trp Leu Pro Ile Gly Cys Ala Ala Phe Val Val Val
```

```
          140                 145                 150

tgc att ttg gga tgc ata ctt att tgt tgg ctt aca aaa aag aag tat      532
Cys Ile Leu Gly Cys Ile Leu Ile Cys Trp Leu Thr Lys Lys Lys Tyr
    155                 160                 165

tca tcc agt gtg cac gac cct aac ggt gaa tac atg ttc atg aga gca      580
Ser Ser Ser Val His Asp Pro Asn Gly Glu Tyr Met Phe Met Arg Ala
170                 175                 180                 185

gtg aac aca gcc aaa aaa tct aga ctc aca gat gtg acc cta               622
Val Asn Thr Ala Lys Lys Ser Arg Leu Thr Asp Val Thr Leu
                190                 195

taatatggaa ctctggcacc caggcatgaa gcacgttggc cagttttcct caacttgaag    682
tgcaagattc tcttatttcc gggaccacgg agagtctgac ttaactacat acatctttctg    742
ctggtgtttt gttcaatctg gaagaatgac tgtatcagtc aatggggatt ttaacagact    802
gccttggtac tgccgagtcc tctcaaaaca aacaccctct tgcaaccagc tttggagaaa    862
gcccagctcc tgtgtgctca ctgggagtgg aatccctgtc tccacatctg ctcctagcag    922
tgcatcagcc agtaaaacaa acacatttac aagaaaaatg ttttaaagat gccaggggta    982
ctgaatctgc aaagcaaatg agcagccaag gaccagcatc tgtccgcatt tcactatcat   1042
actacctctt ctttctgtag ggrtgagaat tcctctttta atcagtcaag ggagatgctt   1102
caaagctggr gctattttat ttctgagatg ttgatgtgaa ctgtacatta gtacatactc   1162
agtactctcc ttcaattgct gaaccccagt tgaccatttt accaagactt tagatgcttt   1222
cttgtgccct caatttttctt tttaaaaata cttctacatg actgcttgac agcccaacag   1282
ccactctcaa tagagagcta tgtcttacat tctttcctct gctgctcaat agttttatat   1342
atctatgcat acatatatac acacatatgt atataaaatt cataatgaat atatttgcct   1402
atattctccc tacaagaata tttttgctcc agaaagacat gttcttttct caaattcagt   1462
taaaatggtt tactttgttc aagttagtgg taggaaacat tgcccggaat tgaaagcaaa   1522
tttawwttat tatcctattt tctaccatta tctatgtttt catggtgcta ttaattacaa   1582
gtttagttct ttttgtagat catattaaaa ttgcaaacaa aatcatcttt aatgggccag   1642
cattctcatg gggtagagca gaatattcat ttagcctgaa agctgcagtt actataggtt   1702
gctgtcagac tatacccatg gtgcctctgg gcttgacagg tcaaaatggt ccccatcagc   1762
ctggagcagc cctccagacc tgggtggaat tccagggttg agagactccc ctgagccaga   1822
ggccactagg tattcttgct cccagaggct gaagtcaccc tgggaatcac agtggtctac   1882
ctgcattcat aattccagga tctgtgaaga gcacatatgt gtcagggcac aattccctct   1942
cataaaaacc acacagcctg gaaattggcc ctggcccttc aagatagcct tctttagaat   2002
atgatttggc tagaaagatt cttaaatatg tggaatatga ttattcttag ctggaatatt   2062
ttctctactt cctgtctgca tgcccaaggc ttctgaagca gccaatgtcg atgcaacaac   2122
atttgtaact ttaggtaaac tgggattatg ttgtagttta acattttgta actgtgtgct   2182
tatagtttac aagtgagacc cgatatgtca ttatgcatac ttatattatc ttaagcatgt   2242
gtaatgctgg atgtgtacag tacagtacwt aacttgtaat ttgaatctag tatggtgttc   2302
tgttttcagc tgacttggac aacctgactg gctttgcaca ggtgttccct gagttgtttg   2362
caggtttctg tgtgtggggt ggggtatggg gaggagaacc ttcatggtgg cccacctggc   2422
ctggttgtcc aagctgtgcc tcgacacatc ctcatcccaa gcatgggaca cctcaagatg   2482
aataataatt cacaaaattt ctgtgaaatc aaatccagtt ttaagaggag ccacttatca   2542
aagagatttt aacagtagta agaaggcaaa gaataaacat ttgatattca gcaactgaaa   2602
aaaaaaaa                                                           2610
```

<210> 4
<211> 2072
<212> DNA
<213> Rattus norvegicus

<220>
<221> CDS
<222> (35)...(634)

<400> 4

```
ctggagggga agagtgcagc tgttcctggc agac atg aag ccc tac ttc tcg tgc      55
                                    Met Lys Pro Tyr Phe Ser Cys
                                     1               5

gtc ttt gtc ttc tgc ttc cta atc aaa ctt tta aca gga gaa ctc aat      103
Val Phe Val Phe Cys Phe Leu Ile Lys Leu Leu Thr Gly Glu Leu Asn
         10                  15                  20

gac ttg gcc aat cac agg atg ttt tcg ttt cac gat gga ggt gta cag      151
Asp Leu Ala Asn His Arg Met Phe Ser Phe His Asp Gly Gly Val Gln
     25                  30                  35

att tct tgt aac tac cct gag act gtc cag cag tta aaa atg cag ttg      199
Ile Ser Cys Asn Tyr Pro Glu Thr Val Gln Gln Leu Lys Met Gln Leu
 40                  45                  50                  55

ttc aaa gac aga gaa gtc ctc tgc gac ctc acc aag acc aag gga agc      247
Phe Lys Asp Arg Glu Val Leu Cys Asp Leu Thr Lys Thr Lys Gly Ser
                 60                  65                  70

gga aac acc gtg tcc atc aag aat ccg atg tcc tgt cca tat cag ctg      295
Gly Asn Thr Val Ser Ile Lys Asn Pro Met Ser Cys Pro Tyr Gln Leu
             75                  80                  85

tcc aac aac agt gtc tct ttt ttc cta gac aac gca gac agc tcc cag      343
Ser Asn Asn Ser Val Ser Phe Phe Leu Asp Asn Ala Asp Ser Ser Gln
         90                  95                 100

ggc agc tac ttt tta tgc agc ctg tcg att ttc gac cca ccc cct ttt      391
Gly Ser Tyr Phe Leu Cys Ser Leu Ser Ile Phe Asp Pro Pro Pro Phe
    105                 110                 115

caa gaa aag aac ctt agt gga gga tat ttg ctt att tat gaa tcc cag      439
Gln Glu Lys Asn Leu Ser Gly Gly Tyr Leu Leu Ile Tyr Glu Ser Gln
120                 125                 130                 135

ctt tgt tgc cag ctg aag ctt tgg tta ccc gta ggg tgt gca gct ttt      487
Leu Cys Cys Gln Leu Lys Leu Trp Leu Pro Val Gly Cys Ala Ala Phe
                140                 145                 150

gtg gca gcg ctc ctt ttt gga tgc ata ttt atc gtc tgg ttt gca aaa      535
Val Ala Ala Leu Leu Phe Gly Cys Ile Phe Ile Val Trp Phe Ala Lys
            155                 160                 165

aag aag tac aga tcc agt gtg cac gac cct aat agc gag tac atg ttc      583
Lys Lys Tyr Arg Ser Ser Val His Asp Pro Asn Ser Glu Tyr Met Phe
        170                 175                 180

atg gcg gca gtc aac aca aac aaa aag tcc aga ctt gca ggt atg acc      631
Met Ala Ala Val Asn Thr Asn Lys Lys Ser Arg Leu Ala Gly Met Thr
    185                 190                 195

tca taatctggaa cacgggaacc catggaggaa ctacactgtc tagttcccct          684
Ser
200
```

```
gaaacttgaa tggagaaagt cttctatttt ctggaccaca gggcatctga cttgattaac    744
tactgatacc tccttttggk gttttgtttg tctggatcag tgactatcag tcactcggaa    804
tttcagcaga ctgccctggg tttgctgagt cctttttaagg caaaccccct cttatagaag    864
acccggctca tatgtattca acaaacagac cttactggga tacaatcccc tctttctgcg    924
cctgcttcta gctatgcacc ggccagcaag acaaacatat ctccagcatt tttacaaaaa    984
tgccagggta tgaatctgta aagtacacag gcagccattg accaccgtct gtcctcgttt   1044
tttcagattc tatttttttc catagagatc agcattcctt ctagaatcag acagtagagg   1104
gagatgcttc acaacagaag ctcttatgtt tctgagatgt tgatgaattc atgctttagt   1164
accaccatgt tctctaacaa cttctatatt ccagctgatc actgcttcag ggcttagatg   1224
cctgcttttg ccttcaagtc tccccttaaa gatactccca caggtctact tggtggcctg   1284
cagccactct gaataggaag tttggtctac aatttccccc ctctgctgct caaaaaaaaa   1344
aattagtaga tatgattttc ccatattctc cctgccaaag taatttttc cagcaaagac   1404
atctaaattc agttaatatg gtttactgtg ttgatattag tggcagtaaa catttctcag   1464
aatcaaaagc aaattaattt tgcggtggtg tttttctacc attatcttgg gtttccatgg   1524
tgctattact cacaagttta gctatttttt tatgcatcat attaaagttg caagcaagca   1584
gagcaaccct cggttaatgg gcaaacattc tcctggggta gaatgaattg tctatttagc   1644
ccgaaaactg cagtttctgt gggtggctgc cagactacag ccgtgctttg ctctggcttt   1704
gacaggttga aatagycccc atgascstgg aacagwactc cagactgtgc tggagtccca   1764
aagttaggag ggccatggag cctgggacag gctgctgctt tggtctttag gatctaggaa   1824
raattacaga ggggccaaga cagagttccc tcccctagaa actgtgcagc ctggaagtca   1884
gccctggcac tttaagatag ccttctttag aacatgagtt agttggtagt attctgacgt   1944
gtaaacagcc tatkgttgct cggagctgga ccatttttct cacttccctg tctgcatgcc   2004
taagacttct agagcagcca acgtatatgc aacattaaag aaaaaaaaaa aaaaaaaaaa   2064
aaaaaaaa                                                           2072
```

<210> 5
<211> 603
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)...(600)

<400> 5

```
atg aag ccg tac ttc tgc cat gtc ttt gtc ttc tgc ttc cta atc aga      48
Met Lys Pro Tyr Phe Cys His Val Phe Val Phe Cys Phe Leu Ile Arg
 1               5                  10                  15

ctt tta aca gga gaa atc aat ggc tcg gcc gat cat agg atg ttt tca      96
Leu Leu Thr Gly Glu Ile Asn Gly Ser Ala Asp His Arg Met Phe Ser
            20                  25                  30

ttt cac aat gga ggt gta cag att tct tgt aaa tac cct gag act gtc     144
Phe His Asn Gly Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val
        35                  40                  45

cag cag tta aaa atg cga ttg ttc aga gag aga gaa gtc ctc tgc gaa     192
Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu
    50                  55                  60

ctc acc aag acc aag gga agc gga aat gcg gtg tcc atc aag aat cca     240
Leu Thr Lys Thr Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro
65                  70                  75                  80

atg ctc tgt cta tat cat ctg tca aac aac agc gtc tct ttt ttc cta     288
```

```
Met Leu Cys Leu Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
                 85                  90                  95

aac aac cca gac agc tcc cag gga agc tat tac ttc tgc agc ctg tcc      336
Asn Asn Pro Asp Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser
            100                 105                 110

att ttt gac cca cct cct ttt caa gaa agg aac ctt agt gga gga tat      384
Ile Phe Asp Pro Pro Pro Phe Gln Glu Arg Asn Leu Ser Gly Gly Tyr
        115                 120                 125

ttg cat att tat gaa tcc cag ctc tgc tgc cag ctg aag ctc tgg cta      432
Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu
    130                 135                 140

ccc gta ggg ttg cca gct ttc gtt gtg gta ctc ctt ttt gga tgc ata      480
Pro Val Gly Leu Pro Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile
145                 150                 155                 160

ctt atc atc tgg ttt tca aaa aag aaa tac gga tcc agt gtg cat gac      528
Leu Ile Ile Trp Phe Ser Lys Lys Lys Tyr Gly Ser Ser Val His Asp
                165                 170                 175

cct aat agt gaa tac atg ttc atg gcg gca gtc aac aca aac aaa aag      576
Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys
            180                 185                 190

tct aga ctt gca ggt gtg acc tca taa                                 603
Ser Arg Leu Ala Gly Val Thr Ser
        195                 200
```

<210> 6
<211> 836
<212> DNA
<213> Rattus norvegicus

<220>
<221> CDS
<222> (35)...(682)

<400> 6

```
ctggagggga agagtgcagc tgttcctggc agac atg aag ccc tac ttc tcg tgc      55
                                       Met Lys Pro Tyr Phe Ser Cys
                                        1               5

gtc ttt gtc ttc tgc ttc cta atc aaa ctt tta aca gga gaa ctc aat      103
Val Phe Val Phe Cys Phe Leu Ile Lys Leu Leu Thr Gly Glu Leu Asn
         10                  15                  20

gac ttg gcc aat cac agg atg ttt tcg ttt cac gat gga ggt gta cag      151
Asp Leu Ala Asn His Arg Met Phe Ser Phe His Asp Gly Gly Val Gln
     25                  30                  35

att tct tgt aac tac cct gag act gtc cag cag tta aaa atg cag ttg      199
Ile Ser Cys Asn Tyr Pro Glu Thr Val Gln Gln Leu Lys Met Gln Leu
 40                  45                  50                  55
```

```
ttc aaa gac aga gaa gtc ctc tgc gac ctc acc aag acc aag gga agc      247
Phe Lys Asp Arg Glu Val Leu Cys Asp Leu Thr Lys Thr Lys Gly Ser
                60                  65                  70

gga aac acc gtg tcc atc aag aat ccg atg tcc tgt cca tat cag ctg      295
Gly Asn Thr Val Ser Ile Lys Asn Pro Met Ser Cys Pro Tyr Gln Leu
            75                  80                  85

tcc aac aac agt gtc tct ttt ttc cta gac aac gca gac agc tcc cag      343
Ser Asn Asn Ser Val Ser Phe Phe Leu Asp Asn Ala Asp Ser Ser Gln
        90                  95                  100

ggc agc tac ttt tta tgc agc ctg tcg att ttc gac cca ccc cct ttt      391
Gly Ser Tyr Phe Leu Cys Ser Leu Ser Ile Phe Asp Pro Pro Pro Phe
    105                 110                 115

caa gaa aag aac ctt agt gga gga tat ttg ctt att tat gaa tcc cag      439
Gln Glu Lys Asn Leu Ser Gly Gly Tyr Leu Leu Ile Tyr Glu Ser Gln
120                 125                 130                 135

ctt tgt tgc cag ctg aag ctt tgg tta ccc gta ggg tgt gca gct ttt      487
Leu Cys Cys Gln Leu Lys Leu Trp Leu Pro Val Gly Cys Ala Ala Phe
                140                 145                 150

gtg gca gcg ctc ctt ttt gga tgc ata ttt atc gtc tgg ttt gca aaa      535
Val Ala Ala Leu Leu Phe Gly Cys Ile Phe Ile Val Trp Phe Ala Lys
            155                 160                 165

aag aag tac aga tcc agt gtg cac gac cct aat agc gag tac atg ttc      583
Lys Lys Tyr Arg Ser Ser Val His Asp Pro Asn Ser Glu Tyr Met Phe
        170                 175                 180

atg gcg gca gtc aac aca aac aaa aag tcc aga ctt gca ggt aca gca      631
Met Ala Ala Val Asn Thr Asn Lys Lys Ser Arg Leu Ala Gly Thr Ala
    185                 190                 195

ccc ctt agg gct ttg ggg aga gga gaa cac tct tca tgt caa gac cgg      679
Pro Leu Arg Ala Leu Gly Arg Gly Glu His Ser Ser Cys Gln Asp Arg
200                 205                 210                 215

aat taatttgttt atttctattt taaaagaaag acatttttte ccctaaagat          732
Asn

aatttttgta tttttatgtg aaagtctgaa tcttcatttt aactcgactt atatactctg   792
tggtatatta aaaataatgt ttgtgaaaaa aaaaaaaaaa aaaa                    836
```

<210> 7
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> primer for PCR

<400> 7

ctgctcgaga tgaagcccta ctttctcg 28

<210> 8
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> primer for PCR

<400> 8
accctacggg taacggatcc ttcagctggc aa 32

<210> 9
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> primer for PCR

<400> 9
taactgtttc tcgagaacat gaagtcaggc 30

<210> 10
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> primer for PCR

<400> 10
atcctatggg taacggatcc ttcagctggc 30

<210> 11
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> primer for PCR

<400> 11
cgtgatattg ctgaagagct tggcggcgaa tgggc 35

<210> 12
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> primer for PCR

<400> 12
cattcaagtt tcagggaact agtccatgcg tttc 34

<210> 13
<211> 200
<212> PRT
<213> Rattus norvegicus

<400> 13
Met Lys Pro Tyr Phe Ser Cys Val Phe Val Phe Cys Phe Leu Ile Lys
1 5 10 15
Leu Leu Thr Gly Glu Leu Asn Asp Leu Ala Asn His Arg Met Phe Ser
20 25 30
Phe His Asp Gly Gly Val Gln Ile Ser Cys Asn Tyr Pro Glu Thr Val
35 40 45
Gln Gln Leu Lys Met Gln Leu Phe Lys Asp Arg Glu Val Leu Cys Asp
50 55 60
Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Asn Pro
65 70 75 80
Met Ser Cys Pro Tyr Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
85 90 95
Asp Asn Ala Asp Ser Ser Gln Gly Ser Tyr Phe Leu Cys Ser Leu Ser
100 105 110
Ile Phe Asp Pro Pro Pro Phe Gln Glu Lys Asn Leu Ser Gly Gly Tyr
115 120 125
Leu Leu Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu
130 135 140
Pro Val Gly Cys Ala Ala Phe Val Ala Ala Leu Leu Phe Gly Cys Ile
145 150 155 160
Phe Ile Val Trp Phe Ala Lys Lys Lys Tyr Arg Ser Ser Val His Asp
165 170 175
Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys
180 185 190
Ser Arg Leu Ala Gly Met Thr Ser
195 200

<210> 14
<211> 200
<212> PRT
<213> Mus musculus

<400> 14
Met Lys Pro Tyr Phe Cys His Val Phe Val Phe Cys Phe Leu Ile Arg
1 5 10 15
Leu Leu Thr Gly Glu Ile Asn Gly Ser Ala Asp His Arg Met Phe Ser
20 25 30
Phe His Asn Gly Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val
35 40 45
Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu
50 55 60
Leu Thr Lys Thr Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro
65 70 75 80
Met Leu Cys Leu Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
85 90 95
Asn Asn Pro Asp Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser
100 105 110
Ile Phe Asp Pro Pro Pro Phe Gln Glu Arg Asn Leu Ser Gly Gly Tyr
115 120 125
Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu
130 135 140

```
Pro Val Gly Leu Pro Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile
145                 150                 155                 160
Leu Ile Ile Trp Phe Ser Lys Lys Lys Tyr Gly Ser Ser Val His Asp
                165                 170                 175
Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys
            180                 185                 190
Ser Arg Leu Ala Gly Val Thr Ser
        195                 200

<210> 15
<211> 216
<212> PRT
<213> Rattus norvegicus

<400> 15
Met Lys Pro Tyr Phe Ser Cys Val Phe Val Phe Cys Phe Leu Ile Lys
 1               5                  10                  15
Leu Leu Thr Gly Glu Leu Asn Asp Leu Ala Asn His Arg Met Phe Ser
            20                  25                  30
Phe His Asp Gly Gly Val Gln Ile Ser Cys Asn Tyr Pro Glu Thr Val
        35                  40                  45
Gln Gln Leu Lys Met Gln Leu Phe Lys Asp Arg Glu Val Leu Cys Asp
    50                  55                  60
Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Asn Pro
65                  70                  75                  80
Met Ser Cys Pro Tyr Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
                85                  90                  95
Asp Asn Ala Asp Ser Ser Gln Gly Ser Tyr Phe Leu Cys Ser Leu Ser
            100                 105                 110
Ile Phe Asp Pro Pro Pro Phe Gln Glu Lys Asn Leu Ser Gly Gly Tyr
        115                 120                 125
Leu Leu Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu
    130                 135                 140
Pro Val Gly Cys Ala Ala Phe Val Ala Ala Leu Leu Phe Gly Cys Ile
145                 150                 155                 160
Phe Ile Val Trp Phe Ala Lys Lys Lys Tyr Arg Ser Ser Val His Asp
                165                 170                 175
Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys
            180                 185                 190
Ser Arg Leu Ala Gly Thr Ala Pro Leu Arg Ala Leu Gly Arg Gly Glu
        195                 200                 205
His Ser Ser Cys Gln Asp Arg Asn
    210                 215

<210> 16
<211> 200
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<221> VARIANT
<222> (1)...(200)
<223> Xaa = Any Amino Acid

<400> 16
```

```
Met Lys Pro Tyr Phe Xaa Xaa Val Phe Val Phe Cys Phe Leu Ile Lys
 1               5                  10                  15
Leu Leu Thr Gly Glu Xaa Asn Xaa Xaa Ala Asn His Arg Met Phe Ser
            20                  25                  30
Phe His Xaa Gly Gly Val Gln Ile Ser Cys Xaa Tyr Pro Glu Thr Val
        35                  40                  45
Gln Gln Leu Lys Met Gln Leu Phe Lys Xaa Arg Glu Val Leu Cys Asp
    50                  55                  60
Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Asn Pro
65                  70                  75                  80
Met Xaa Cys Xaa Tyr Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
                85                  90                  95
Xaa Asn Xaa Asp Ser Ser Gln Gly Ser Tyr Xaa Xaa Cys Ser Leu Ser
            100                 105                 110
Ile Phe Asp Pro Pro Pro Phe Gln Glu Xaa Asn Leu Ser Gly Gly Tyr
        115                 120                 125
Leu Xaa Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu
    130                 135                 140
Pro Val Gly Cys Ala Ala Phe Val Xaa Xaa Leu Leu Phe Gly Cys Ile
145                 150                 155                 160
Xaa Ile Xaa Trp Phe Xaa Lys Lys Lys Tyr Xaa Ser Ser Val His Asp
                165                 170                 175
Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys
            180                 185                 190
Ser Arg Leu Ala Gly Xaa Thr Xaa
        195                 200
```

<210> 17
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<221> VARIANT
<222> (1)...(214)
<223> Xaa = Any Amino Acid

<400> 17

```
Met Leu Xaa Leu Xaa Leu Ala Trp Xaa Leu Xaa Leu Phe Xaa Leu Xaa
 1               5                  10                  15
Ile Xaa Val Xaa Xaa Xaa Xaa Ile Xaa Val Xaa Gln Xaa Xaa Xaa Xaa
            20                  25                  30
Xaa Ala Xaa Xaa Asn Gly Xaa Xaa Xaa Xaa Xaa Cys Lys Tyr Xaa Xaa
        35                  40                  45
Pro Xaa Xaa Xaa Xaa Glu Phe Arg Xaa Xaa Leu Leu Lys Gly Xaa Asp
    50                  55                  60
Ser Xaa Val Xaa Xaa Cys Xaa Xaa Xaa Xaa Thr Tyr Xaa Xaa Gly Asn
65                  70                  75                  80
Xaa Val Xaa Xaa Lys Xaa Xaa Xaa Xaa Cys Xaa Gly Xaa Leu Ser Asn
                85                  90                  95
Asn Ser Val Xaa Phe Xaa Leu Gln Asn Leu Xaa Xaa Xaa Xaa Thr Xaa
            100                 105                 110
Xaa Tyr Phe Cys Lys Xaa Glu Xaa Met Tyr Pro Pro Pro Tyr Xaa Xaa
        115                 120                 125
Xaa Xaa Xaa Asn Gly Thr Xaa Ile His Val Xaa Xaa Xaa Xaa Leu Cys
```

```
    130                 135                 140
Pro Xaa Xaa Xaa Phe Xaa Xaa Trp Xaa Leu Xaa Xaa Val Xaa Xaa Xaa
145                 150                 155                 160
Leu Xaa Xaa Tyr Ser Xaa Leu Xaa Thr Ala Xaa Ile Xaa Xaa Xaa Xaa
                165                 170                 175
Xaa Lys Lys Arg Ser Xaa Leu Xaa Xaa Gly Xaa Tyr Met Xaa Met Xaa
            180                 185                 190
Pro Xaa Xaa Pro Xaa Xaa Xaa Xaa Lys Xaa Xaa Gln Pro Tyr Xaa Xaa
        195                 200                 205
Asp Phe Xaa Xaa Xaa Xaa
    210
```

<210> 18
<211> 6
<212> PRT
<213> Homo sapiens

<400> 18
Met Tyr Pro Pro Pro Tyr
 1   5

<210> 19
<211> 4
<212> PRT
<213> Homo sapiens

<400> 19
Tyr Met Asn Met
 1

<210> 20
<211> 4
<212> PRT
<213> Homo sapiens

<400> 20
Tyr Val Lys Met
 1

<210> 21
<211> 6
<212> PRT
<213> Homo sapiens

<400> 21
Phe Asp Pro Pro Pro Phe
 1   5

<210> 22
<211> 4
<212> PRT
<213> Homo sapiens

<400> 22
Tyr Met Phe Met
 1

<210> 23
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<221> VARIANT
<222> (1)...(216)
<223> Xaa = Any Amino Acid

<400> 23
Met Lys Pro Tyr Phe Ser Cys Val Phe Val Phe Cys Phe Leu Ile Lys
 1   5   10   15
Leu Leu Thr Gly Glu Leu Asn Asp Leu Ala Asn His Arg Met Phe Ser
            20   25   30
Phe His Asp Gly Gly Val Gln Ile Ser Cys Asn Tyr Pro Glu Thr Val
        35   40   45
Gln Gln Leu Lys Met Gln Leu Phe Lys Asp Arg Glu Val Leu Cys Asp
    50   55   60
Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Asn Pro
65   70   75   80
Met Ser Cys Pro Tyr Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
                85   90   95
Asp Asn Ala Asp Ser Ser Gln Gly Ser Tyr Phe Leu Cys Ser Leu Ser
            100   105   110
Ile Phe Asp Pro Pro Pro Phe Gln Glu Lys Asn Leu Ser Gly Gly Tyr
        115   120   125
Leu Leu Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu
    130   135   140
Pro Val Gly Cys Ala Ala Phe Val Ala Ala Leu Leu Phe Gly Cys Ile
145   150   155   160
Phe Ile Val Trp Phe Ala Lys Lys Lys Tyr Arg Ser Ser Val His Asp
                165   170   175
Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys
            180   185   190
Ser Arg Leu Ala Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        195   200   205
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
    210   215

<210> 24
<211> 16
<212> PRT
<213> Rattus norvegicus

<400> 24
Leu Arg Ala Leu Gly Arg Gly Glu His Ser Ser Cys Gln Asp Arg Asn
 1   5   10   15

<210> 25
<211> 220
<212> PRT
<213> Homo sapiens

<400> 25

```
Met Leu Arg Leu Leu Leu Ala Leu Asn Leu Phe Pro Ser Ile Gln Val
 1               5                  10                  15
Thr Gly Asn Lys Ile Leu Val Lys Gln Ser Pro Met Leu Val Ala Tyr
            20                  25                  30
Asp Asn Ala Val Asn Leu Ser Cys Lys Tyr Ser Tyr Asn Leu Phe Ser
        35                  40                  45
Arg Glu Phe Arg Ala Ser Leu His Lys Gly Leu Asp Ser Ala Val Glu
    50                  55                  60
Val Cys Val Val Tyr Gly Asn Tyr Ser Gln Gln Leu Gln Val Tyr Ser
65                  70                  75                  80
Lys Thr Gly Phe Asn Cys Asp Gly Lys Leu Gly Asn Glu Ser Val Thr
                85                  90                  95
Phe Tyr Leu Gln Asn Leu Tyr Val Asn Gln Thr Asp Ile Tyr Phe Cys
            100                 105                 110
Lys Ile Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser
        115                 120                 125
Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro
    130                 135                 140
Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly
145                 150                 155                 160
Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile
                165                 170                 175
Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met
            180                 185                 190
Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro
        195                 200                 205
Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
    210                 215                 220
```

<210> 26
<211> 223
<212> PRT
<213> Homo sapiens

<400> 26

```
Met Ala Cys Leu Gly Phe Gln Arg His Lys Ala Gln Leu Asn Leu Ala
 1               5                  10                  15
Ala Arg Thr Trp Pro Cys Thr Leu Leu Phe Phe Leu Leu Phe Ile Pro
            20                  25                  30
Val Phe Cys Lys Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala
        35                  40                  45
Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly
    50                  55                  60
Lys Ala Tyr Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln
65                  70                  75                  80
Val Thr Glu Val Cys Ala Ala Thr Tyr Met Thr Gly Asn Glu Leu Thr
                85                  90                  95
Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val
            100                 105                 110
Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile
        115                 120                 125
Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly
    130                 135                 140
Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser
145                 150                 155                 160
Asp Phe Leu Leu Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe
                165                 170                 175
```

```
Tyr Ser Phe Leu Leu Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys
                180                 185                 190
Arg Ser Pro Leu Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu
        195                 200                 205
Pro Glu Cys Glu Lys Gln Phe Gln Pro Tyr Phe Ile Pro Ile Asn
    210                 215                 220
```